

	2661		2730
humPMS2	(2574)	G ATTCTCAGAAC-----	
AtPMS2	(2267)	G TTA T CTCA C ATTACCTGATGACGACAATGTCAATGATGATGATGATGATGCAACCATCTCATTGGC	
Consensus	(2661)	C TT CTCA A	
	2731		
humPMS2	(2587)	----	
AtPMS2	(2337)	ATGA	
Consensus	(2731)		

Figure 1. Alignment between human PMS2 (humPMS134) and *Arabidopsis thaliana* homologue of PMS2 (AtPMS2) DNA sequences. Similarity is 48.1%; identity is 48.1%. Black boxes show identical nucleotides.

1	70	
humPMS2	(1) --MERABESSTEPAKAIKPIDRKSVHQCICSGQVVISLSIAVKELVENSLDAGATNIDLKLKDYGVLIEV	
AtPMS2	(1) MQGDSSESPTTTSSPLIRPILNRRNVIHRICSGQVILDLSSAVKELVENSLDAGATSIENLIRDGEYFCV	
Consensus	(1) D A S S T A I K P I R I H I C S G Q V I L L S S A V K E L V E N S L D A G A T I D I L K D Y G D V	
	71	140
humPMS2	(69) SDNGCCEVEENF-----EGITLWHTHTSKIQEFADLTQVEFEGFRGEALSSLCAISDVIISCHA	
AtPMS2	(71) IDNGCGISPTNPKVCVQILRRTFDVIALWHTHTSKILEDFTICLNLITFEGFRGEALSSLCALGNLIVERTK	
Consensus	(71) DNGCGI NF D L L K H H T S K I D F D L N L T F G F R G E A L S S L C A L L T I T	
	141	210
humPMS2	(128) SAKVGRMFDFDINGKIIQKTPYPFPRTGTVSVOQLFSTLPVVRHKEFRNIKKEYAKMQLHAYCISAC	
AtPMS2	(141) NEPVAVLITTEDESGLLTAEKKTARQIQTITTVRKLFSNLPVRSKEFRNIKKEYGKLSLUNAVALAKC	
Consensus	(141) VAT L FDH G I R GTTVSV LFS LPVR KEF RNKKEYAKLV LL AY IIA G	
	211	280
humPMS2	(198) IRVSCINQLCQGKROPVVCTGGSFSIKEYIGSVFQOKQLOSLIPFVQLPPSDSVCEEYGLSCSDALHNLF	
AtPMS2	(211) VRFVCSITTCGKPNPKSVLNLQGRGSILKDNITVRCISTFTSQP-----	
Consensus	(211) IR CSN G K VL T G SIKDNI SVFG SL P	
	281	350
humPMS2	(268) YISGFISQCTHVGCRSSTDQFFFINRRCDPAKVCRLVNEVYHMYNRHOYFVVLNISVDSECVIINV	
AtPMS2	(255) ---G-----TCRNLADRQYFFINGRVDMPKUSKLVNELYKDTSRKYPVTTIDFIVPGGACINV	
Consensus	(281) G GR DRQFFFIN RP D KV KLVNELY YP IL V DINVT	
	351	420
humPMS2	(338) PDKRQILLOEEKLLLAVLKTSLIGMFDSVNKLNVSQQPLLDVEGNLIKMHAADLEKPMVEKQDQSPSLR	
AtPMS2	(314) PDKRKVFFSDET-----SV-----	
Consensus	(351) PDKR I DE	
	421	490
humPMS2	(408) TGEKKDVSISRLREAFSLRHTTENKPHSPKTPEPRRSPLGQKRGMLSSSTSGAISDKGVIRPOKEAVSS	
AtPMS2	(328) -----IGSLREGLNEIYSSSNASYIVNRFEENSEQPDKAGVSSFPKKSNLSEGIVLVDVSSKTRLG	
Consensus	(421) I LREA HSS N H E S ISD VL	
	491	560
humPMS2	(478) SHGSPSDPTDRAEVEKDSGHGSTSVDSSEGFSIPDTGSHOSSEYAASSSPCDRGSQEHVDSQEKAPETDSSFS	
AtPMS2	(389) EAIEKENPLSLREVEIDNSSPMEKFKEIACGTTKKGEGSLSVHDVTHLDKTPSKGLPQLNVTEKVIDASK	
Consensus	(491) D EVE D E A S S DK L DA	
	561	630
humPMS2	(548) DVDCHSNQEDTGCKERVLPQPTNLATPNTIRFKKEEILSSSDICQKLVNTQDMASASQVDWAVKINKKVVIP	
AtPMS2	(459) DLSSRSS-----FAQSTLNIFVITMGKREHENISTILSETPVLRNQTSSYRVEKSKFEDRALASRCLME	
Consensus	(561) DL S F T L K ILS S I S M S DV K LV	
	631	700
humPMS2	(618) IEFSSMSSLAKRIKQLHHBAQQSEGEONYRKFRAKICPGENQAAEDELRKEISKTMFAEMEIIGQFNLGFI	
AtPMS2	(522) GQOLDDDMVISKEDMTPSERDSELENRISPGTQA-----D-----NVERHERVLGQFNLGFI	
Consensus	(631) D L K E G A M IIGQFNLGFI	
	701	770
humPMS2	(688) IITKLNEIDIFIVDCHATDEKYNFEMIQQHVIQGQRIIAQTIINTAVNEAVLILENLEIPEKNGEDFVIDE	
AtPMS2	(573) IIAKLERDIDIFIVDQHAADENFNFEEHLARSCLVNOQPLIOPLNLELSPEEEVTVLHMIDIEENGFLLENP	
Consensus	(701) I KL DIFIVDQHA DEKFNFE L TVLN Q LI P L LS E LI LDI R NGF	
	771	840
humPMS2	(758) IAPVTERAKLISLFTSKNWFQPCDVEFPMISDSPCVMCR-----PSRVKQMFASACRK	
AtPMS2	(643) SAPPGKHFTRRAIISYSKNEIFGVEILKD-----STEGNHHGECCSVASSYKTSKTDSCPSRVRAMLASACRS	
Consensus	(771) AP KL AIP SKN TFG DL DLI L D G PSRVK M ASRACR	
	841	907
humPMS2	(815) SVMIGTAINTSEWKKLITIIGEMEDHPWNCPHGRPIMRHIANGVISQN-----	
AtPMS2	(713) SVMICDPKRNEMQKIVELIADLESFWNCPHGRPTMRHLVDTTLLTLPPDDNVNDDDDDATISLA	
Consensus	(841) SVMIG L EM KII HLAQDL PWNCPHGRPTMRHI L I	

Figure 2. Alignment between human PMS2 (humPMS134) and *Arabidopsis thaliana* homologue of PMS2 (AtPMS2) amino acid sequences. Similarity is 41.5%; identity is 31.1%. Black boxes show identical residues.

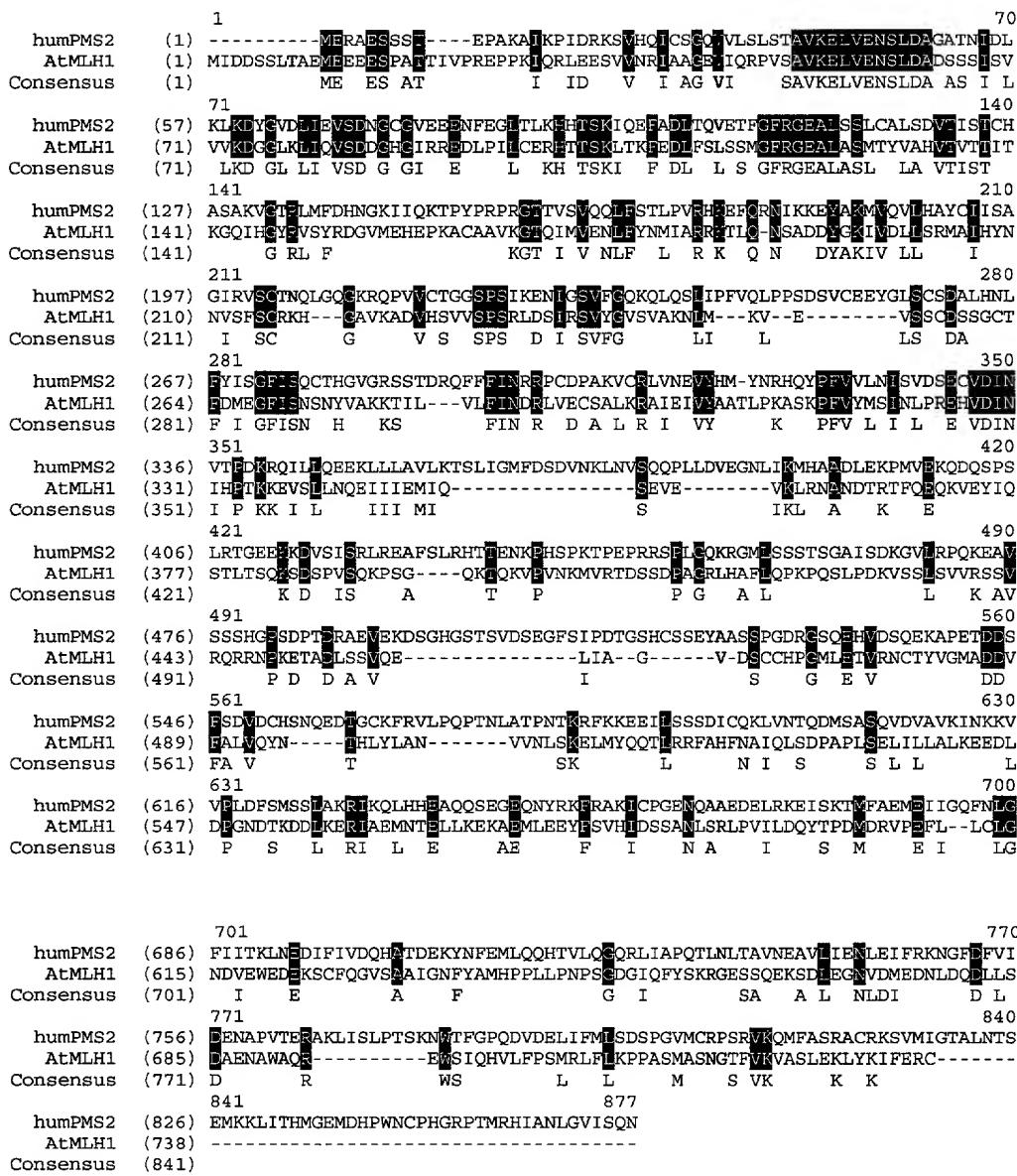


Figure 3. Alignment between human PMS2 (humPMS2) and *Arabidopsis thaliana* PMS2 homologue MLH1 (AtMLH1) amino acid sequences. Similarity is 30%; identity is 18.4%. Black boxes show identical residues.

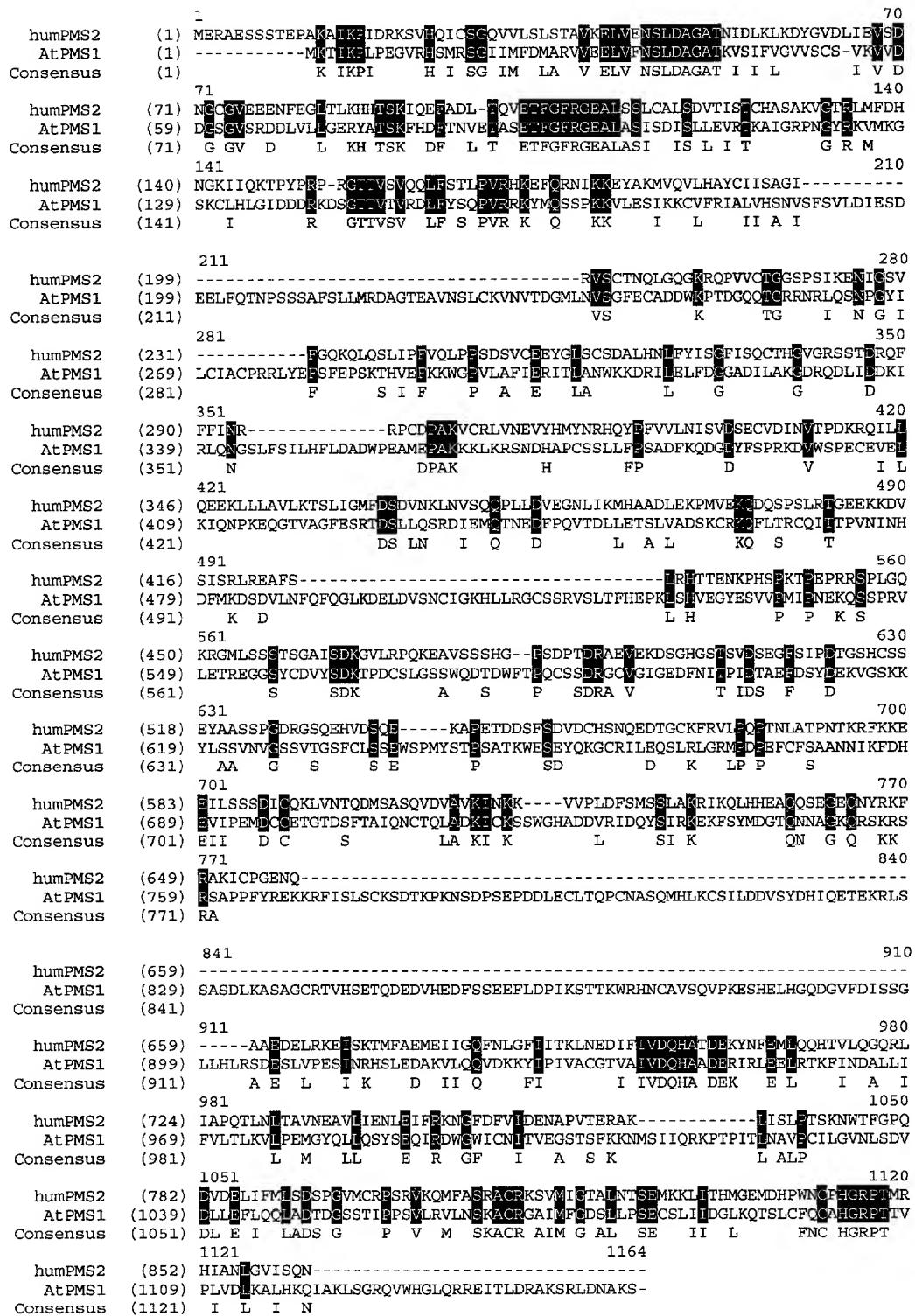


Figure 4. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS1 (AtPMS1) amino acid sequences. Similarity is 24.4%; identity is 15%. Black boxes show identical residues.

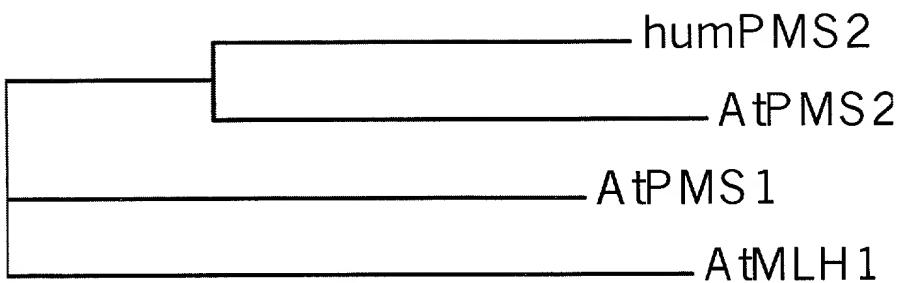


Figure 5. Phylogenetic tree of the *Arabidopsis thaliana* PMS2 gene homologues.

humPMS134	(1) ATCG CGGAGCTGAGAGCTCGAGTACAGAACCTGCTAAGGC-----	70
AtPMS134	(1) ATCGAGGAGATCTTCTCGCTCGGACACTAGCTCCCTTGATAGACCTATAACAGAACG	
Consensus	(1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA	
	71	140
humPMS134	(65) CAGTCCATCAGATTTCGCTTGGGCAGGTGCTACTGAGTCGAAGCACTGGGTAAAGGACTTAGTAGAAAAA	
AtPMS134	(71) TAATTCACAGAACATCTGCTCGGTCAGTCATCTAGACCTCTCTTGCCCTCAAGGACCTTCCTCGAGAA	
Consensus	(71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA	
	141	210
humPMS134	(135) CAGTCTGGATGCTGGTGCCTACTAATTGATCTAAAGCTTAAGGACTATGGACTGGATCTTATTGAGTT	
AtPMS134	(141) TAGTCCTGGACGGCGGCCACCATAGAGATTAACTCCGAGACTACGCCAAAGACTATTTCAGGTC	
Consensus	(141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT	
	211	280
humPMS134	(205) TCA GACAATGGATGTGGGT-----	
AtPMS134	(211) ATTGA CAATGGTTGTGCCATTCCCCAACCATTTCAAGGTTGTCCAAATTCCCGAAGAACCTTTG	
Consensus	(211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT	
	281	350
humPMS134	(251) -----CTCTGAAACATCACAGACTAAAGATTCAAGACCTTGCGCGACCTAACCTGGTTGAA-ACTT	
AtPMS134	(281) ATGTTCTGCACTTAAAGCATCATACTCTAAATTACAGGATTCAGAGATCTT-CTGATTTGACTACTT	
Consensus	(281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT	
	351	420
humPMS134	(311) TTGGCTTTCGGGGAGGCTCTGAGCTCACTTTGTGCACTCGAGCAATGTCACCAATTCTACCTC-CAC	
AtPMS134	(350) ATGGTTTAGAGGAGAACAGGCTTGAGCTCTCTGTCATTCGAAATCTCACTCTGGAAAGAACAAACAAA	
Consensus	(351) TGG TTT G GG GAAGC TGAGCTC CT TGTCGA TG G AT TCAC T AC G C A	
	421	444
humPMS134	(379) GCAATCGGGAGGTCTGAACT---	
AtPMS134	(420) GAAATGAGCCA-GTTGCTAGGCTC	
Consensus	(421) G AT GC A GTTG AC	

Figure 6. Alignment between human PMS134 (humPMS134) and *Arabidopsis thaliana* homologue of PMS134 (AtPMS134) DNA sequences. Similarity is 53.2%; identity is 53.2%. Black boxes show identical nucleotides.

	1	70
humPMS134	(1) --MERAESSSTEPAKAKKEPDIRKSVHOICSGQVVISLSTAVKELVENSLDAGATN	DLKLKDYGVDLIEV
AtPMS134	(1) MQGDSSESPTESSPLRPINENVIHRICSGQVILDLSSAVKELVENSLDAGAT	SEINLRDYQEDYFQV
Consensus	(1) D A S S T A IKPI R IH ICSGQVIL LSSAVKELVENSLDAGAT	IDI LKDYG D V
	71	140
humPMS134	(69) SDNGCCEVEENF-----EGLTALKHHTSKIQEFADITQVEF	GFRGEALSSLCALSDVETISTCHA
AtPMS134	(71) IDNGCGISPTNEKVCVQILRRTFDVLALKHHTSKILEDFTDILNLITY	GFRGEALSSLCALGNLAVETRHK
Consensus	(71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSLCAL	LTI T
	141	
humPMS134	(128) SAKVGL	
AtPMS134	(141) NEPVAT	
Consensus	(141) VAT	

Figure 7. Alignment between human PMS134 (humPMS134) and *Arabidopsis thaliana* homologue of PMS134 (AtPMS134) amino acid sequences. Similarity is 65.1%; identity is 50.7%. Black boxes show identical residues.

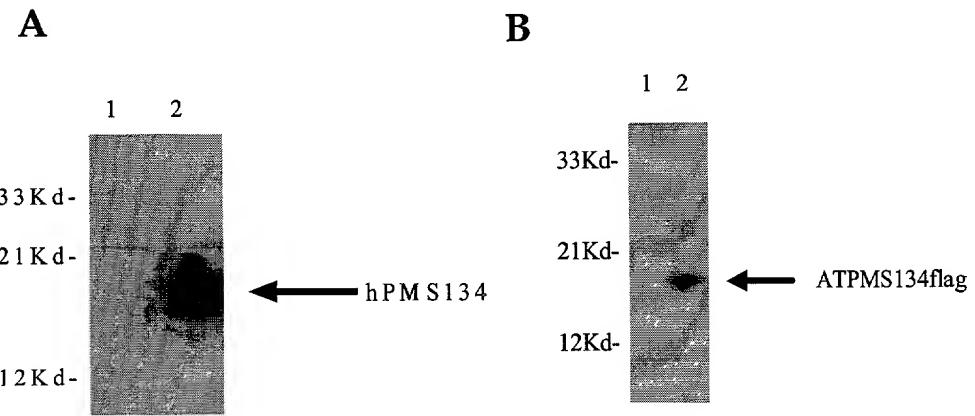


Figure 8: Western blot analysis of bacteria expressing the human PMS134 dominant negative gene (Panel A, lane 2) or the *Arabidopsis thaliana* dominant negative gene (Panel B, lane 2). Panel A, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the human PMS2 N-terminus. Panel B, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the flag epitope placed on the C-terminus of the *Arabidopsis* PMS134 gene. Lane 1 is bacteria containing empty vector as negative control

Dominant Negative Effects of *Arabidopsis thaliana* PMS2 homolog

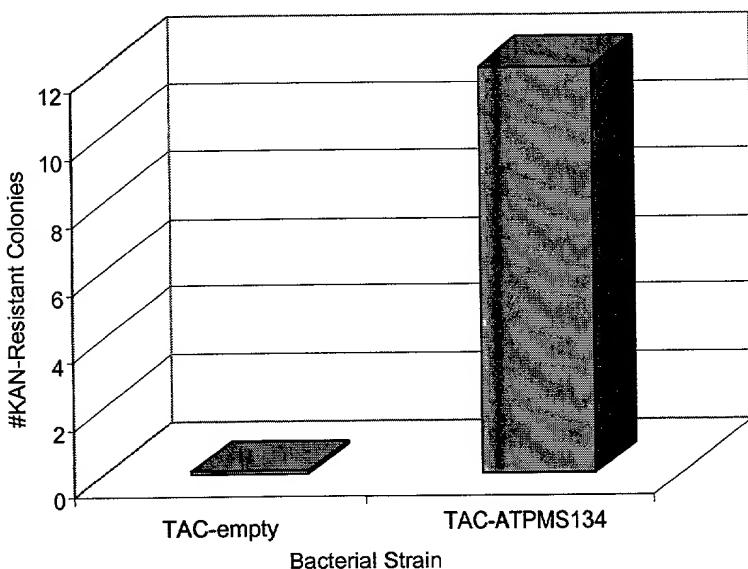


Figure 9. Expression of the *Arabidopsis thaliana* PMS134 gene produces hypermutability in bacteria leading to the generation of new phenotypes. Briefly, bacteria containing the empty vector or the TAC ATPMS134 expression vector were grown and plated on kanamycin containing Lbagar plates. The host bacteria are susceptible to KAN bactericidal activity. Bacterial cultures expressing the hPMS134 gene resulted in genetic alteration of the bacterial host and the generation of clones that are KAN resistant.

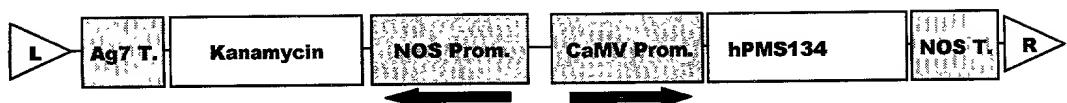


Figure 10. Schematic map of the pCMV-hPMS134-Kan binary plant expression vector. Ag7 T. and NOS T. = gene 7 and Nopaline Synthase poly(A) signals, respectively. NOS Prom and CaMV Prom = Nopaline Synthase and Cauliflower Mosaic Virus promoters, respectively. L and R = left and right T-DNA border repeats, respectively. Arrows indicate direction of transcription.

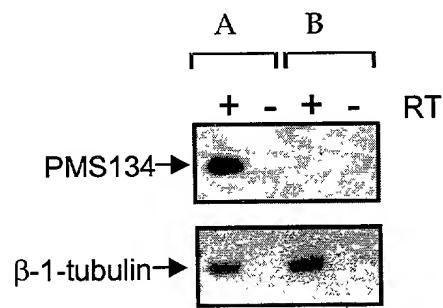


Figure 11. Expression of hPMS134 in *Arabidopsis Thailana*. Message analysis for T1 plants shows steady state expression of dominant negative MMR genes in PMS134-Kan plants (A) while none is observed in control plants (B). Tubulin was used as an internal control to monitor sample loading and integrity.

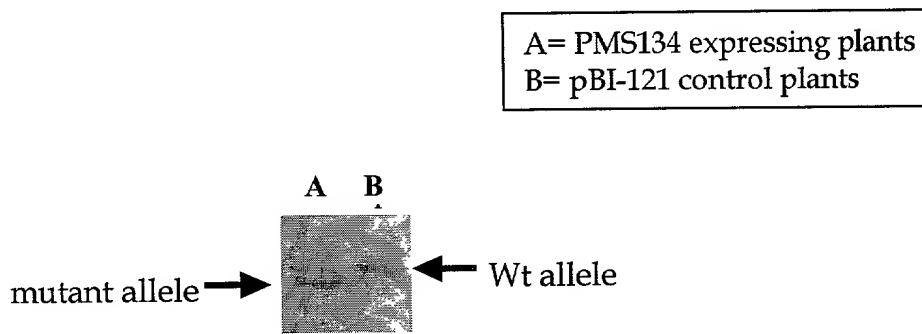


FIGURE 12. Expression of PMS134 expression causes MI in plants. Microsatellite analysis of Nga280 in PMS134 expressing plants (Lane A) found the generation of a mutant allele in contrast to control plants (Lane B).

Figure 13. The plant on the left is a wild type *A. thaliana* and the one on the right is MMR defective. Seeds from the MMR defective plant have been obtained and offspring have the same “double-meristem” trait.

